

TGGCCGCTCTGGCTCTGAGCAGCGTCGCAGAGGCCTCCCTGGGCTCCGCGCGCAGCCCTGCCCCCGCGAAGGCCCCCCGCCTGTCCTGGCGTC 100 W P L W L C . A A S Q R P P W A P R P A A L P P A K A P R L S W R GGGGCGGCCGGTGGACGGCCCATCCACTCTCCCCGCTCCCCCGCCCCGACCGGGCCCTGTGGCGCGCACTGACCCAGAGTAAGGTCCCCCTGCGTG PPPATCRVGERARGRGGAGPGHRA.LGLIPGGRT 300 ARW CSGRARPPPQPSRPAPPPSALPRG G RNA A R A G G P G S R A R A A G A R G C R L R S Q L V P V R A L G TGGCCACCGCTCCGACGAGCTGGTGCGTTTCCGCTTCTGCAGCGGCTCCTGCCGCCGCGCGCCTCTCCACACGACCTCAGCCTGGCCAGCCTACTGGG L G H R S D E L V R F R F C S G S C R R A R S P H D L S L A S L L G ···· M CGCCGGGGCCCTGCGACCCCCGGGCTCCCGGCCCGTCAGCCCTGCTGCCGACCCCACGCGCTACGAAGCGGTCTCCTTCATGGACGTCAACAGC 600 AGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNS ACCTGGAGACCGTCTCCGCCACCGCCTGCGGCTGCGTGGGCTGAGGGCTCCCAGGGCTTTGCAGACTGGACCCTTACCGGTGG 696 T W R T V D R L S A T A C G C L G . G L A P G L C R L D P Y R W

FIGURE 1A

ATG	SAA	CTI	GGA	CT?	rgg.	AG	GCC	TC:	rcc	ACG	СТ	GTC	CCZ	ACT	GCC	cc	TGGC	СТ	'AGC	GCG	GC	AGC	СТ	GCC	СТ	GTG	GC	CCP	CC	СТС	GC	CG	CTC	TG	GCI	'CT	GCT	GA	
TAC	CTT	GAA	CCT	GA/	ACC'	TC	CGG	AG/	AGG	TGC	GA	CAG	GGT	∵ rga	CGG	GG	ACCO	GA	ATC	CGC	CG:	rcg	GA	CGG	GAG	CAC	CG	GGI	'GG	GAC	CG	GC:	GAG	+ I AC	CGA	→+ \GA	.CGA	+ CT	100
м •••	E	L	G • •	L	G I • •	• •	G 	L	s + • •	т 	L	S • • •	S 1	н •••	С	P	w	P	R	R	. (⊋ • + •	P	A +++	L	₩ • + •	7	P	т	L +	A	• •	A	L +	Α	L ++	L	· •+	
GCA	SCG	STCG	CAG	AGO	GCC'	TC	CCT	GGG	GCT	'CCG	CG	CCC	CGG	CAG	ccc	TG	cccc	cc	CGC	GAA	GGG	ccc	:CC	CGC	CTO	GTC	СТ	GGC	GT	ccc	cc	GC	CGG	CC	ACC	TG:	CCG	GG	200
CGT	CGC	AGC	GTC	TC	CGG	AG	GGA	CC	CGA	.GGC	GC	GGG	GC	STC	GGG	AC	GGGG	GG	GCG	CTT	CCC	GGG	GG	GCG	GA	CAG	GA	CCG	CA	GGG	GG	CG	GCC	GG	TGG	AC	GGC	CC	
s :	S • → •	.V	А • •	E	A +++	s	L 	• •	G I ⊶	s 	A	P • • •	R	s +	·	· · · · · ·	A E	› - -	R	E	G	₽ + + •	•	P • • •	P	∨ • • •	L	. F		s ++	P	A ++	G	; ++	H	L ++	P	G + 	
GGG	ACG	CAC	GGC	cco	GCT(GG'	rgc	AG'	rgg	AAC	SAG	CCC	GGG	CGG	CCC	cc	GCCG	C.P	AGC	СТТ	CTC	cgg	cc	CGC	GC	ccc	CG	CCG	CC'	TGC	CAC	CC	CCA	TC	TGC	TC	TTC	cc	
CCC	rgc	GTO	CCG	GG	CGA	CC	ACG	TC	ACC	ттс	CTC	GGG	CCC	GCC	GGC	GG	cGGC	GI	CGC	GAA	GA	GCC	GG	GCG	CG	GGG	GC	GGC	GG	ACC	TG	GG	GGT	'AG	ACC	→ I GAG	AAG	GG	300
G.	F	₹ 7	' A		R '	W • • •	c · ·	s	G	; F	₹	A • • • •	R	R → 	P	E F	P	, +	2 1	P ↔	s	R • ∔•	P	- A	. :	P + -	P	P	P	. F	<u> </u>	P ++	P	s • I		\ +	L	₽	
CGC	; GG	GGC	:CGC	GC	GGC	GC	GGG	CTO	GGG	GGC	ccc	GGG	CAG	GCC	GCC	CT	'CGGG	GC <i>P</i>	AGC	GGG	GGG	CGC	GG	GGC	TG	CCG	CC.	TGO	:GC	TCG	CA	GC:	TGG	TG	CCG	GT	'GCG	CG	400
_GCG	3CC	CCG	GCG	CG	CCG	CG	CCC	GA	CCC	CCG	GGG	CCC	GT	CGG	CGC	:GA	GCC	GT	rcg	CCC	CCC	GCG	CC	CCG	AC	GGC	GG.	ACC	GCG.	AGC	GT	CG	ACC	AC	GGC	:CA	CGC	→ I :GC	400
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GCG	AGC	CCGG	ACC	CG	I • • GTG	GC	GAG	GC'	rgc	TCC	SAC	CAC	CGC	· · AAA	GGC	GA	AGA	GT	rcg	CCG	AG	- - GAC	GG	CGG	CG	CGC	GC	GAC	AG	+ GTC	TG	CT	GGA	→ I GT	CGG	 SAC	CGG	TC	500
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ATGGAACTGGGACTTGCAGAGCCTACTGCATTGTCCCACTGCCTCCGGCCTAGGTGGCAGTCAGCCTGGTGGCCAACCCTAGCTGTTCTAGCCCTGCTGA TACCTTGACCCTGAACGTCTCGGATGACGTAACAGGGTGACGGAGGCCGGATCCACCGTCAGTCGGACCACCGGTTGGGATCGACAAGATCGGGACGACT MELGLAEPTALSHCLRPRWQSAWWPTLAVLALL S C V T E A S L D P M S R S P A A R D G P S P V L A P P T D H L P G GGGACACACTGCGCATTTGTGCAGCGAAAGAACCCTGCGACCCCGCCTCAGTCTCCTCAGCCCGCACCCCCGCCGCCTGGTCCCGCGCTCCAGTCTCCT G H T A H L C S E R T L R P P P Q S P Q P A P P P G P A L Q S P P A L R G A R A A R A G T R S S R A R T T D A R G C R L R S Q L receestrange of the state of th **ACGGECACTCA**CGCGAGCCGGATCCGGTGTCGAGGCTGCTCGACTATGCAAAGGCGAAGACGTCGCCGAGCACGGCGGCTCGTGCGAGGGTCGTGCTAGA P V S A L G L G H S S D E L I R F R F C S G S C R R A R S Q H D L $\textbf{:} \textbf{AGT} \underline{\underline{\textbf{G}}} \textbf{T} \textbf{GGCCAGCCTACTGGGGCCCTACGGTCGCCTCCCGGGTCCCGGCCGATCAGCCCAGCCCTGCTGCCGGCCCACTCGCTATGAGGCCGTC}$ * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * * | * * * * | * * * * | * * * * | * * * * | * * * | * * * | * * * | * * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * 60 SUL A S L L G A G A L R S P P G S R P I S Q P C C R P T R Y E A V 675

FIGURE 1C

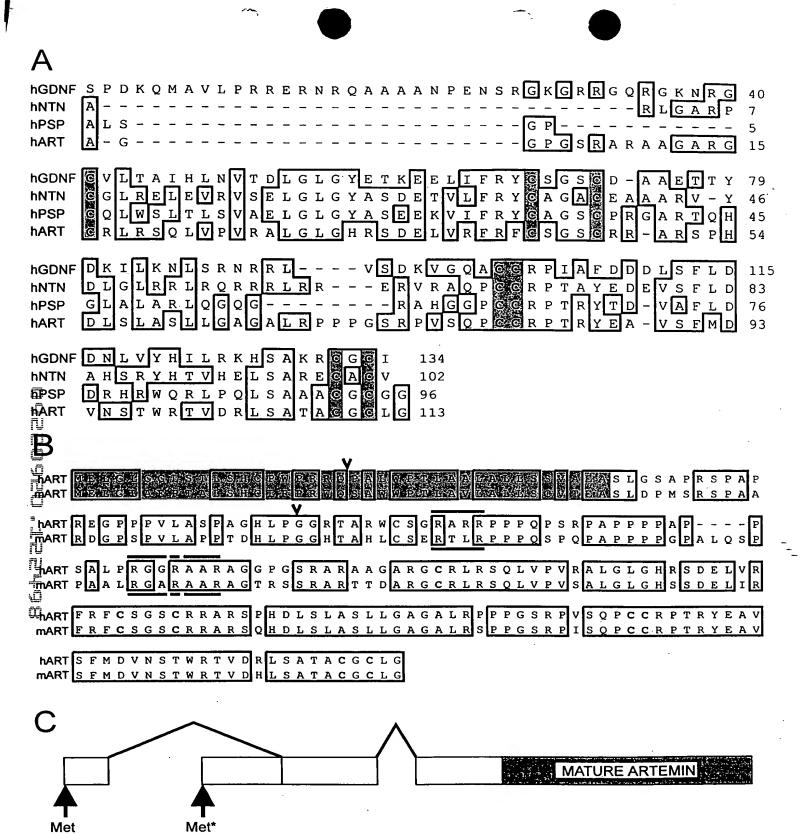
F M D V N S T W R T V D H L S A T A C G C L G

ATGCCCGGCCTGATCTCAGCCCGAGGACAGCCCCTCCTTGAGGTCCTTCCT	100
M P G L I S A R G Q P L L E V L P P Q A H L G A L F L P E A P L	G . ••••
MCMCCCCC CACCCMCCCCCCACCCCCACCCCCCCCCCC	
TCTCCGCGCAGCCTGCCCTGTGGCCCACCCTGGCCGCTCTGGCTCTGAGCAGCGTCGCAGAGGCCTCCCTGGGCTCCGCGCCCCGCAGCCCTC	200
AGAGGCGCGTCGGACGGGACACCGGGGGGCGCGAGACCGAGACGACTCGTCGCAGCGTCTCCGGAGGGACCCGAGGCGCGCGGGGCGTCGGGAC	CGGGG
LSAQPALWPTLAALALSSVAEASLGSAPRSP	A P
CCGCGAAGGCCCCCCGCCTGTCCTGGCGTCCCCCGCCGGCCACCTGCCGGGGGGACGCACGGCCGCTGGTGCAGTGGAAGAGCCCGGCGGCGCCGCCGCCGCCGCCGCCGCCGCC	
GGCGCTTCCGGGGGGGGACAGGACCGCAGGGGGGGGGGG	
	. .
REGPPVLASPAGHLPGGRTARWCSGRARRP	
	•
CAGECTTCTCGGCCCGCGCCCCCCCCCCCCCCCCCCCCCC	
######################################	
©1000010000000000000000000000000000000	AGCCC
Q P S R P A P P P P A P P S A L P R G G R A A R A G G P G S R A	
	+
. 5	
CAGCGGGGCGCGGGCTGCGCTCGCAGCTGGTGCCGGTGCGGCGCGCTCGGCCTGGGCCACCGCTCCGACGAGCTGCTTTCCGC	500
GTCGCCCCCGCGCCCCGACGCGACGCGACCCCACGCCACGCCACGCGACCCGGACCCGGTGGCGAGGCTGCTCGACCACGCAAAGGCG	-
A R G A R G C R L R S Q L V P V R A L G L G H R S D E L V R F R	F C

CAGCGGCTCCTGCCGCGCGCGCCCCCCGGGCTCCCACACGACCTCAGCCTGCCAGCCTACTGGGCGCCCGGGGCCCCCGGGCTCCCGGC	CCGTC
	-
CTCGCCGAGGACGCCGCGCGCGCGAGAGGTGTGCTGGAGTCGGACCGGTCGGATGACCCGCGGGCCCCGGGACGCTGGCGGGGCCCGAGGGCCG	GGCAG
S G S C R R A R S P H D L S L A S L L G A G A L R P P P G S R	P V
	
AGCCAGCCCTGCTGCCGACCCACGCGCTACGAAGCGGTCTCCTTCATGGACGTCAACAGCACCTGGAGAACCGTGGACCGCCTCTCCGCCACCGC	
TCGGTCGGGACGACGGCTGGGTGCGCGATGCTTCGCCAGAGGAAGTACCTGCAGTTGTCGTCGTCGTCGCACCTGGCGGAGAGGCGGTGGCG	
S Q P C C R P T R Y E A V S F M D V N S T W R T V D R L S A T A	
	+
GCTGCCTGGGCTGA	
**************** 714	
CGACGGACCCGACT	

FIGURE 1D

G C L G .



100		200		8			
cerococococococococococococococococococo	AGGPGSRARAGARGCRLRSQLVPVRALGHR	ccgacgagergergegriftecgerrergegegereergeegeegeegegegegerrergeacgearergageerggeegeeragegegegegegeerer 	SDELVRFRFCSGSCRRARSPHDLSLAGAL	GCGACCGCCCCGGGCCTCCGGCCCTCAGCCTGCTGCTGCCGACCCACGCGCTACGAAGCGGTCTCCTTCATGGACGTCAAGAGCACCTGGAGAACC	RPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT	GIGGACCGCCTCTCCGCCACCGCCTGCCTGCCTGA 342	VDRLSATACGCIG.

FIGURE 3A

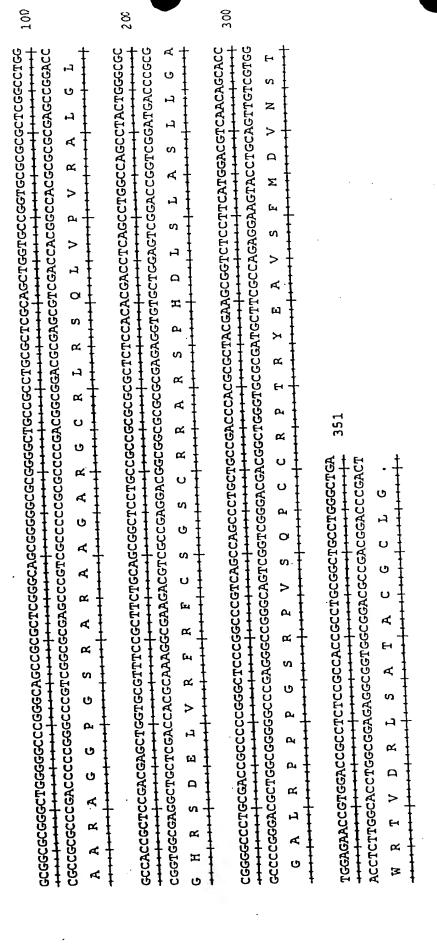
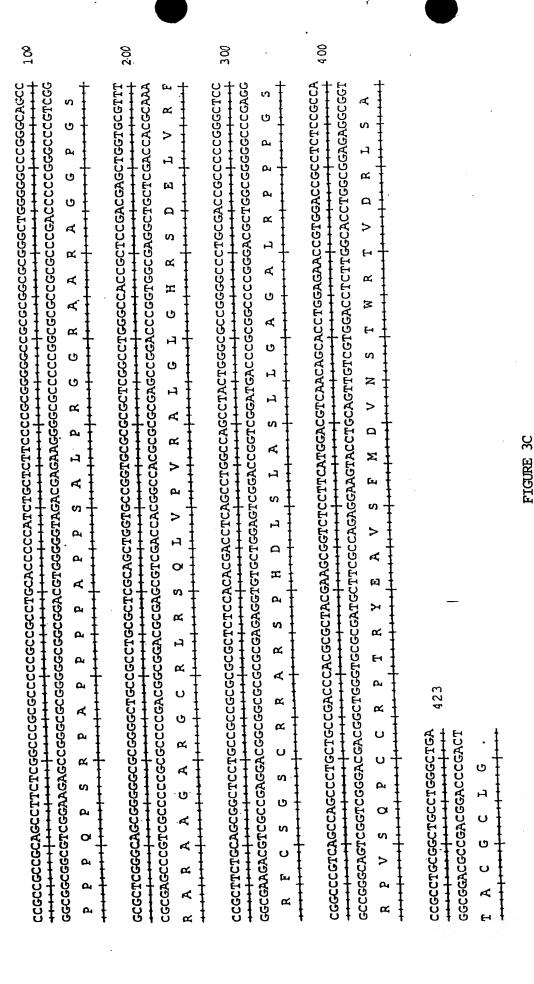
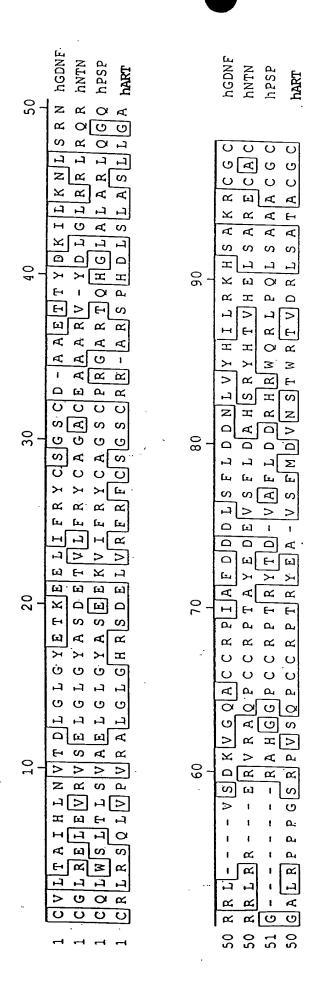
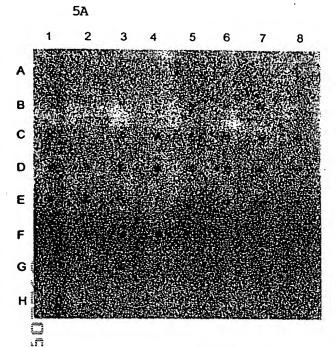


FIGURE 3B





TIGURE A



	1	2	3	4	5	6	7	8
A	whole brain	amygdala	ceudate aucleus	cere- bellum	cerebral cortex	frontal lobe	hippo- campus	medulia oblongata
В	occipital Isba	putamen	substantia nigra	temperal lobe	thalamus	sub- thelemic nucleus	spinal cord	
C	heart	eorta	skeletal muscle	ceton	bladder	sterus	prostate	stomach
D	testis	OASIA	pancreas	pituitery gland	edrena) gland	thyroid gland	sativary gland	mammary gland
E	kidney	liver	small intestine	spices	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta -			-	
G	fetal brein	fetal heart	fetal kidaey	fotal liver	fetal spleen	fetal thymus	fetal lung	
H	years total RNA 100 ng	yeast sRNA 100 ng	£ coll rRNA 100 ng	E coli DNA 100 ag	Poly r(A)	human C _e t 1 DNA 100 ng	kuman DNA 100 ng	human DNA 500 ng

FIGURE 5

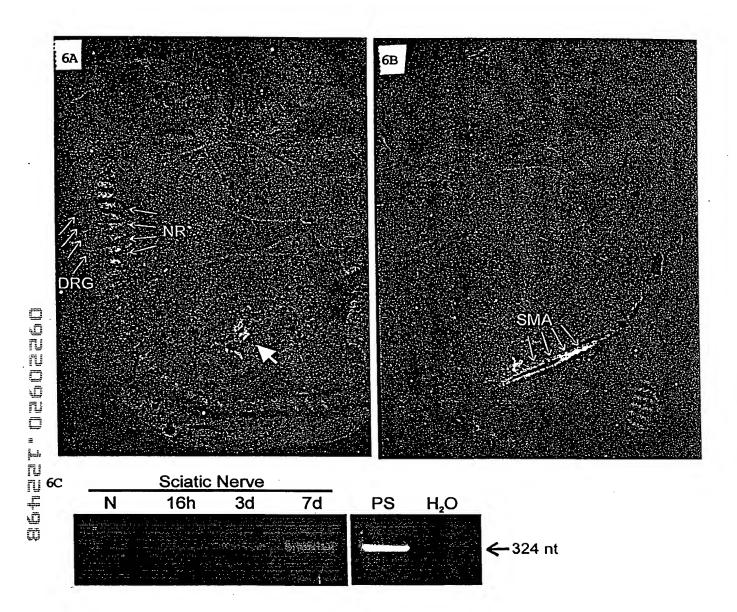


FIGURE 6

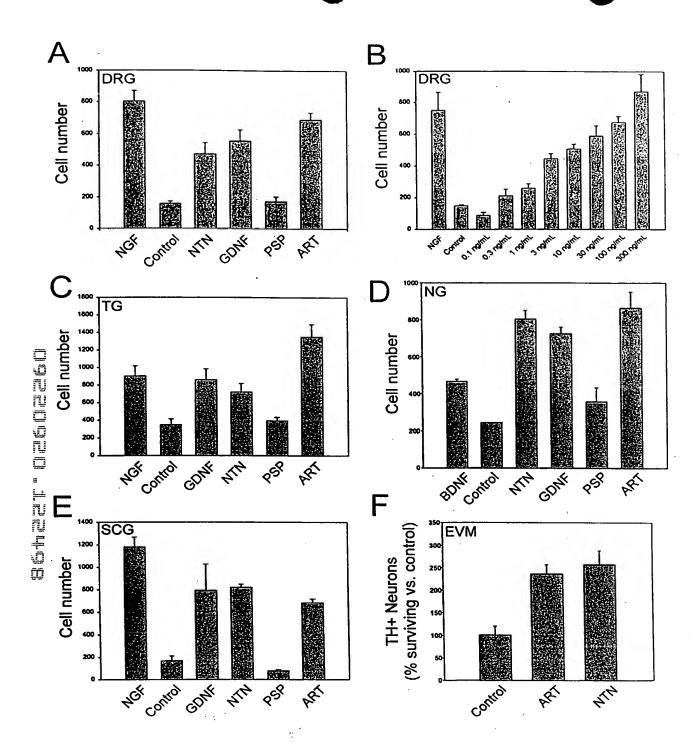


FIGURE 7

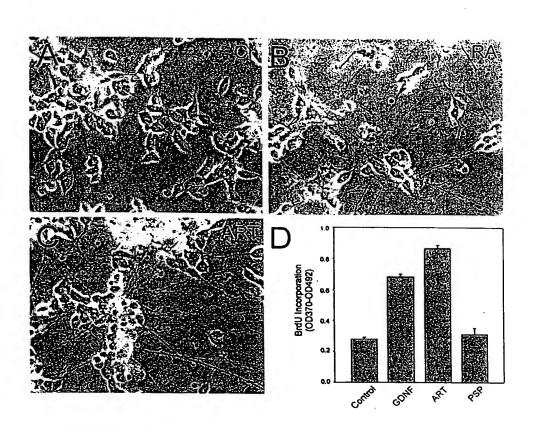


FIGURE 8

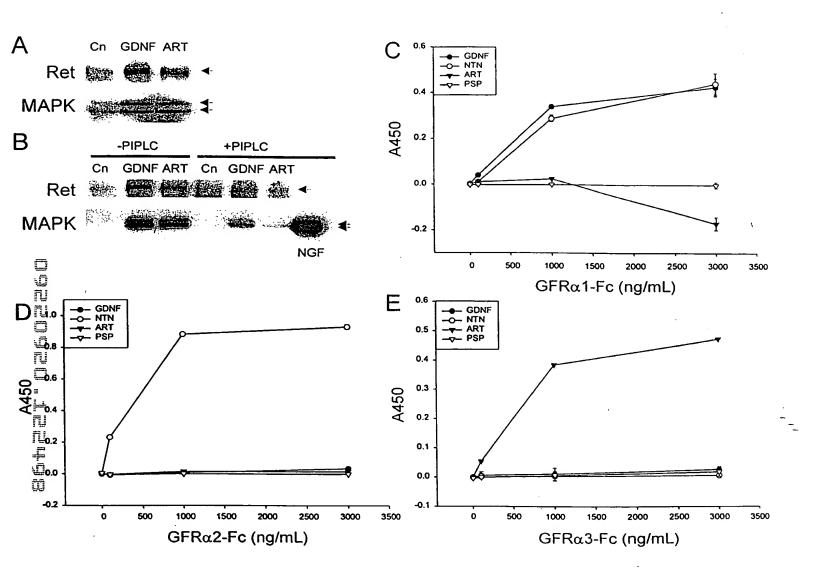
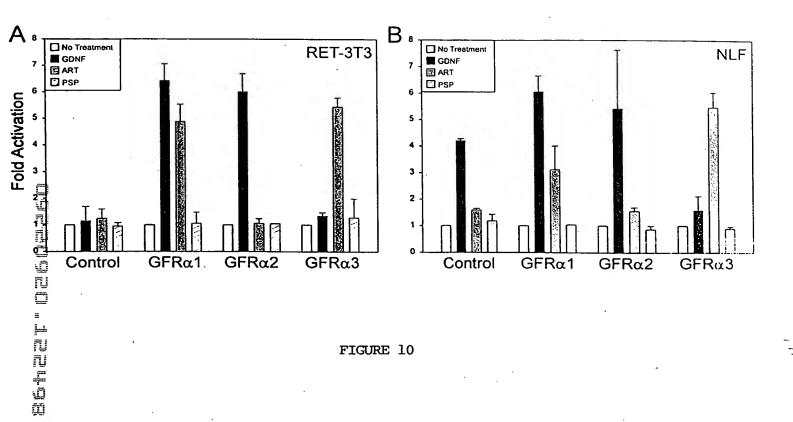


FIGURE 9



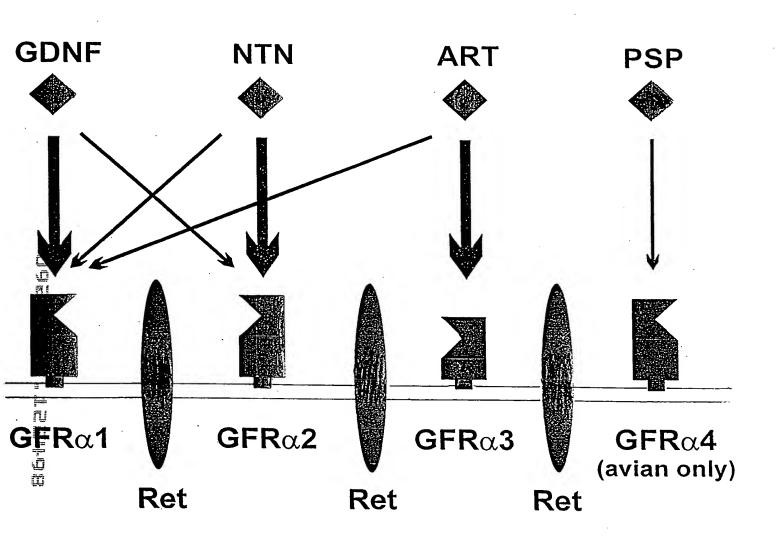


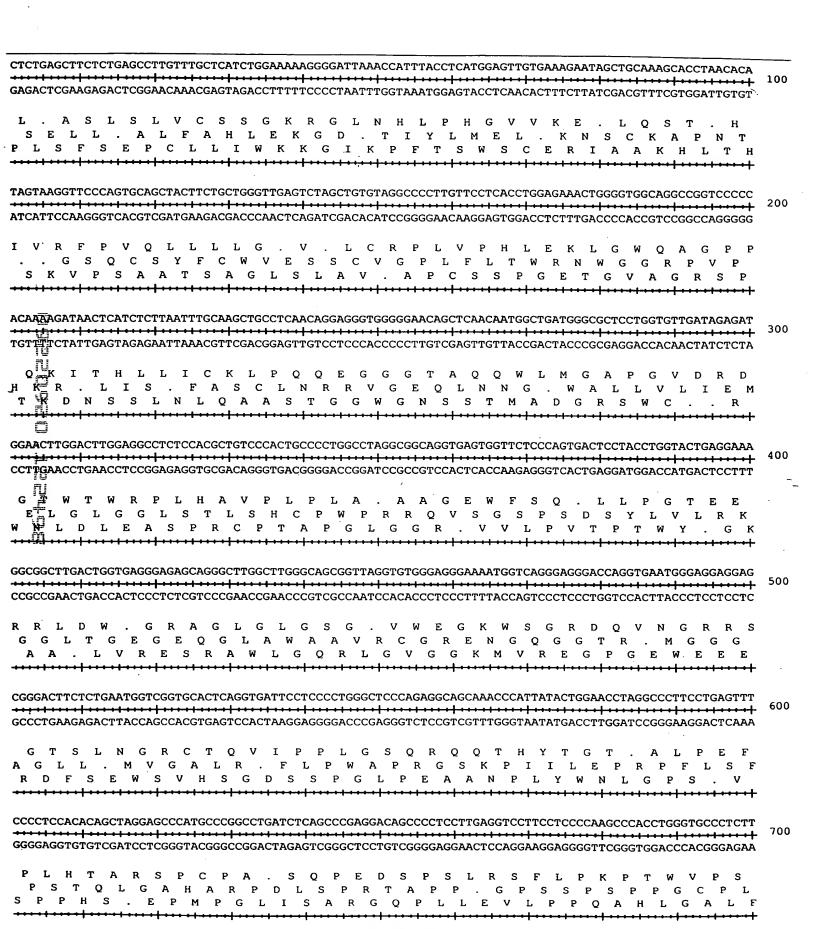
FIGURE 11

hGFRα3 N S C L Q A R R K C Q A D P T C S A A Y H H L D S C T S S I S T P L P S E E P S V mGFRα3 N S C T Q A R K K C E A N P A C K A A Y Q H L G S C T S S L S R P L P L E E S A M hGFRa3 PADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRA mGFRa3 SADCLEAA EQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA hGFRa3 R S L G N Y E L D V S P Y E D T V T S K P W K M N L S K L N M L K P D S D L C L K mGFRa3RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLK hGFRa3FAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQLLTFFE mGFRa3FAMLCTLHDKCDRLRKAYGEACSGIRCORHLCLAOLRSFFE hGFRa3 KAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAP mGFRa3KAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTP hGFRa3 NCLELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEOSR mGFRa3NCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSR hGFRa3 CLRAYLGLIGTAMTPNFVSNVNTSVALSCTCRGSGNLQEEC mGFRa3CLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDEC hGFRa3 EMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVMA mGFRa3EQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQ hGFRa3 HQNENERAVEROREW mGFRa3QQNSNPA

FIGURE 12

TCTCGCAGCCGGAGACCCCCTTCCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGCTG TCGGTCCCTGCTGACTGCCTGGAGGCAGCACACACTCAGGAACAGCTCTCTGATAGGCTGCATGTGCCACCGGCGCAT GAAGAACCAGGTTGCCTTGGACATCTATTGGACCGTTCACCGTGCCCGCAGCCTTGGTAACTATGAGCTGGATGTCT SEGECCCCACTECCAGEGECTOTGCCTCAGGCAGCTGCTCATTTCTTCGAGAAGGCCGCCGAGCCCCCACGCGCAGG CTGCCGCCTGTGGCCCCCCAACTGCCTGGAGCTGCGCGCCTTCTCCCGACCCGCTTTGCAGATCACGCCTGGTGGA TTTCCAGACCCACTGCCATCCCATGGACATCCTAGGAACTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCTGG GGCTGATTGGGACTGCCCATGACCCCCAACTTTGTCAGCAATGTCAACACCCAGTGTTGCCTTAAGCTGCACCTGCCGAGGC AGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGGGTTCTTCTCCCACAACCCCTGCCTCACGGAGGCCATTGCAGC PAGATGCGTTTTCACAGCCAACTCTTCTCCCAGGACTGGCCACACCCTACCTTTGCTGTGATGGCACACCAGAATGAAA ACCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTTTTCTCCTGCACGCTTCCCTTGATTCTGCTCCTGAGCCTATGG CCCCCTATGAAGACACAGTGACCAGCAAACCCTGGAAAATGAATCTCAGCAAACTGAACATGCTCAAACCAGACTCAGAC CTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGACAAGTGTGACCGGCTGCGCAAGGCCTACGGGGAGGCGTGCTC ATCCCACCTGCAGTGCTGCCTACCACCTGGATTCCTGCACCTCTAGCATAAGCACCCCCACTGCCTCAGAGGAGCCT

FIGURE 13



TCTCCCTGAGGCTCCACTTGGTCTCTCCGCGCAGCCTGCCCTGTGGCCCACCCTGGCCGCTCTGGCTCTGAGCAGCGTCGCAGAGGCCTCCCTGGGC 800 AGAGGGACTCCGAGGTGAACCAGAGAGGCGCGTCGGACGGGACACCGGGTGGGACCGGCGAGACCGAGACTCGTCGCAGCGTCTCCGGAGGGACCCG FSLRLHLVSPRSLPCGPPWPLWLC.'AASQRP STWSLRAACPVAHPGRSGSAEQRRRGLPG PEAPLG L S A Q P A L W P T L A A L A L L S S V A E A S L G · · · · · · | · · · · | · · · · | · · · · | · · · · · | · · · · | · · · · | · · · · | · · · · | · · · · | · · · · | · · · · | · · · · · | · · · · · | · · · · · | · · · · · | · · · · · | 900 P R P A A L P P A K A P R L S W R P P P A T C R V G E R A R G R G RAPQPCPPACPGVPRRPPAG.VRGRGGGA A P R S P A P R E G P P P V L A S P A G H L P G R . E G E G A G G P G H R A . L G L I P G G R T A R W C S G R A R R P P P Q P S R P A P P P A P P S A L P R G G R A A R A G G P G S R A R A G FG P R P R R L H P H L L F P A G A A R R G L G A R A A L G Q R S A R A P A A C T P I C S S P R G P R G A G W G P G Q P R S G S G GGCGCGGGGCTGCCGCCTGCGCTCGCAGCTGCTGCCGCTGCGCCCCCTGGGCCACCGCTCCGACGAGCTGGTGCGTTTCCGCTTCTGCAGCGGC A R G C R L R S Q L V P V R A L G L G H R S D E L V R F R F C S G CARSWCRCARSAWAT G A G L P P A L A A G A G A R A R P G P P L R R A G A F P L L Q R S C R R A R S P H D L S L A S L L G A G A L R P P P G S R P V A R A L H T T S A W P A Y W A P G P C D R P R A P G P S A L L P P R A L S T R P Q P G Q P T G R R G P A T A P G L P A R Q P A GGACGACGGCTGGGTGCGCGATGCTTCGCCAGAGGAAGTACCTGCAGTTGTCGTGGACCTCTTGGCACCTGGCGGAGAGGCGGTGGCCGACGCACGACGA C C R P T R Y E A V S F M D V N S T W R T V D R L S A T A C G C L A A D P R A T K R S P S W T S T A P G E P W T A S P P P P A L L P T H A L R S G L L H G R Q Q H L E N R G P P L R H R L R L P

*** * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * * | * * * | * * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * * | * | * * | * * | * | * * | * | * * | * | * * | * | * * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | 150 G . G L A P G L C R L D P Y R W L F L P G T L P Q S P T S Q R P Q W A E G S L Q G F A D W T L T G G S S C L G P S R R V P L A S G L S G L R A R S R A L Q T G P L P V A L P A W D P P A E S H . P A A S 160 P G T K A S K L R G P C R W V M D I I P E Q V K G Q L T S S P R A QGRRPQS.EAPAGG.WISSPNR.RDN.LAAPEP ARDEGLKAERPLPVGDGYHPRTGEGTTD. QPQSP TCACCCTGCGGATCCCAGCCTAAAAGACACCAGAGACCTCAGCTATGGAGCC **AGTGGGACGCCTAGGGTCGGATTTTCTGTGGTCTCTGGAGTCGATACCTCGG** Ш TELRIPA. KTPETSAMEP E C G S Q P K R H Q R P Q L W S PADPSLKDTRDLSYGA Н FIGURE 14C

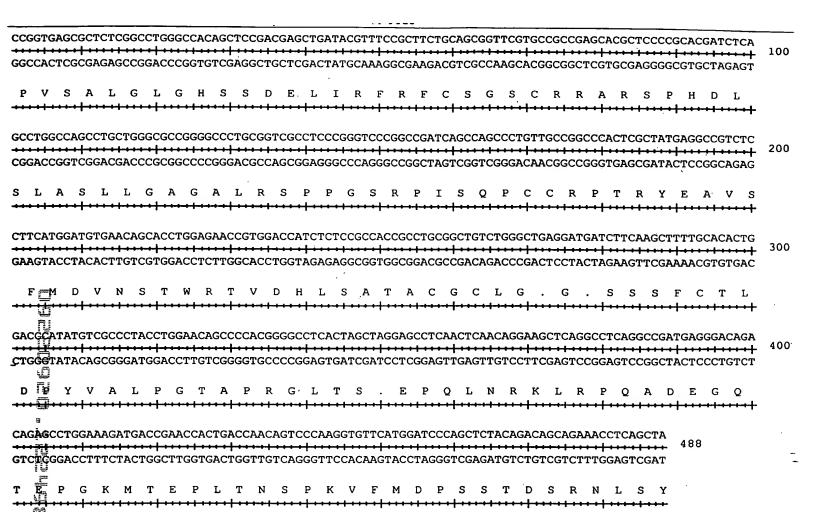


FIGURE 15